

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings of claims in the application:

**Listing of Claims:**

1                   **1-109.** (canceled).

1                   **110.** (previously presented) A thermodynamic method for predicting duplex  
2 stability of an oligonucleotide sequence comprising at least one modified nucleotide base, said  
3 method comprising:

4                   a) providing an oligonucleotide having a sequence of N bases, wherein said  
5 oligonucleotide comprises at least one modified base; and

6                   b) calculating duplex stability of said oligonucleotide using an algorithm applying  
7 a nearest-neighbor model for duplex formation thermodynamics for each of the N-1 neighboring  
8 base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic  
9 contribution of two corresponding neighboring bases.

1                   **111.** (previously presented) A method for predicting the melting temperature  
2 ( $T_m$ ) of an oligonucleotide sequence comprising at least one modified nucleotide base, said  
3 method comprising:

4                   a) providing an oligonucleotide having a sequence of N bases, wherein said  
5 oligonucleotide comprises at least one modified base; and

6                   b) calculating a melting temperature ( $T_m$ ) of said oligonucleotide using an  
7 algorithm applying nearest neighbor thermodynamic parameters for each of the N-1 neighboring  
8 base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic  
9 contribution of two corresponding neighboring bases.

1                   **112.** (previously presented) The method of any one of claims 110 or 111,  
2 wherein said oligonucleotide sequence is derived from a database source.

1                   **113.** (previously presented) The method of claim 112, wherein said  
2 oligonucleotide sequence is derived from Genbank.

1                   **114.** (previously presented) The method of any one of claims 110 or 111,  
2 wherein said at least one modified base is a member selected from the group consisting of a base  
3 attached to an amino acid, a polyamide nucleic acid (PNA) and a locked nucleic acid sugar.

1                   **115.** (previously presented) The method of claim 114, wherein said modified  
2 base is attached to PNA.

**116.** (previously presented) The method of claim 114, wherein said modified  
base a locked nucleic acid sugar.

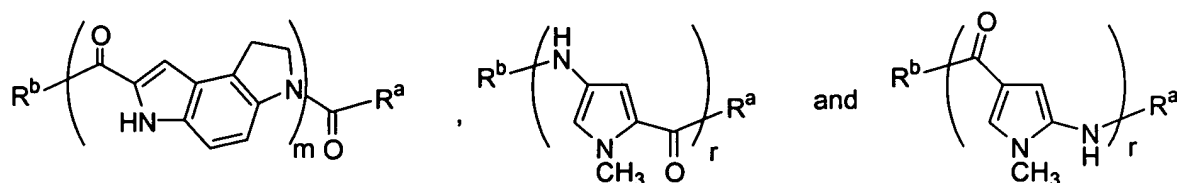
**117.** (currently amended) The method of any one of claims 110 or 111, ~~115 or~~  
~~116~~, wherein said oligonucleotide comprising at least one modified base has superior mismatch  
discrimination, in comparison to unmodified nucleotides.

**118.** (previously presented) The method of any one of claims 110 or 111,  
wherein said at least one modified base is a member selected from the group consisting of a  
universal base, PPA, PPG, PPPA, PPPG, PU, PC, HOPU, HOBuU, HOBuC, (NH<sub>2</sub>)<sub>2</sub>PPPA,  
(NH<sub>2</sub>)<sub>2</sub>PPPAOH, (NH<sub>2</sub>)<sub>2</sub>BuPPAOH, (NH<sub>2</sub>)<sub>2</sub>PPAI, and HOBuPPG.

**119.** (previously presented) The method of any one of claims 110 or 111,  
wherein said oligonucleotide has attached to it one or more members selected from the group  
consisting of a minor groove binder, a fluorophore and a quencher.

**120.** (previously presented) The method of claim 119, wherein said  
oligonucleotide sequence has a minor groove binder attached thereto.

**121.** (previously presented) The method of claim 120, wherein said minor  
groove binder has a formula selected from the group consisting of:



wherein

the subscript  $m$  is an integer of from 2 to 5;

the subscript  $r$  is an integer of from 2 to 10; and

each  $R^a$  and  $R^b$  is independently a linking group to said modified oligonucleotide, H,  $OR^c$ ,  $NR^cR^d$ ,  $COOR^c$  and  $-CONR^cR^d$  wherein each  $R^c$  and  $R^d$  is selected from the group consisting of H,  $(C_1-C_{12})$ heteroalkyl,  $(C_2-C_{12})$ heteroalkenyl,  $(C_2-C_{12})$ heteroalkynyl,  $(C_1-C_{12})$ alkyl,  $(C_2-C_{12})$ alkenyl,  $(C_2-C_{12})$ alkynyl, aryl $(C_1-C_{12})$ alkyl and aryl.

**122.** (previously presented) The method of claim 120, wherein said minor groove binder is attached to the oligonucleotide via a quencher molecule.

**123.** (previously presented) The method of any one of claims 110 or 111, wherein said algorithm predicts the melting temperature ( $T_m$ ) of said oligonucleotide with an accuracy of about  $\pm 2^\circ C$ .

**124.** (previously presented) The method of any one of claims 110 or 111, wherein said method is applied in establishing appropriate conditions for hybridization, renaturation, mapping variations of base compositions of sequences or determination of sequence complexity and divergence.

**125.** (previously presented) The method of any one of claims 110 or 111, wherein said oligonucleotide is a capture probe in an array.

**126.** (new) The method of claim 115, wherein said oligonucleotide comprising at least one modified base has superior mismatch discrimination, in comparison to unmodified nucleotides.

127. (new) The method of claim 116, wherein said oligonucleotide comprising at least one modified base has superior mismatch discrimination, in comparison to unmodified nucleotides.